

GenCore version 5.1.³
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OM protein - protein search, using sw model
Run on: January 9, 2003, 12:23:23 ; Search time 11 Seconds
(without alignments),
49.017 Million cell updates/sec

Title: US-09-632-429-4
Perfect score: 89
Sequence: 1 WEVLCNTWETCER 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.1*

Prob. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	43	48.3	524	1	CP72_CATRO	Q05047 catharanthus roseus L.
2	43	48.3	536	1	KCN1_RAT	P70606 ratius norv
3	43	48.3	580	1	KCN1_MOUSE	Q9egr3 mus musculi
4	42	47.2	561	1	KCN1_HUMAN	P72952 homo sapien
5	42	47.2	569	1	URB1_SYN1	P73061 synchocystis sp.
6	42	47.2	574	1	KCN2_MOUSE	P58390 mus musculi
7	42	47.2	579	1	KCN2_HUMAN	Q9h2s1 homo sapien
8	42	47.2	580	1	KCN2_RAT	P70604 ratius norv
9	42	47.2	724	1	KCN3_PTG	P58392 sus scrofa
10	42	47.2	731	1	KCN3_MOUSE	P70605 ratius norv
11	42	47.2	732	1	KCN3_RAT	Q9ug16 homo sapien
12	42	47.2	736	1	KCN3_HUMAN	P07046 neurospora crassa
13	41.5	46.6	359	1	3SHD_NEUCR	P07046 neurospora crassa
14	41	46.1	236	1	SUR1_RALSO	P83097 drosophila melanogaster
15	41	46.1	236	1	SUR2_RALSO	Q30919 ralstonia eutettii
16	41	46.1	278	1	RRE1_YEAST	P35178 sacharomyces cerevisiae
17	41	46.1	330	1	Q0TG_EMENTI	P25416 emericella
18	41	46.1	340	1	QAX_NEICR	P11634 neurospora crassa
19	41	46.1	416	1	PAN1_XENLA	P49263 xenopus laevis
20	41	46.1	809	1	WSCK_DROME	P83097 drosophila melanogaster
21	40	44.9	295	1	YHR6_YEAST	P38710 sacharomyces cerevisiae
22	40	44.9	741	1	TLE4_RAT	Q07141 ratius norv
23	40	44.9	1080	1	C1A7_HUMAN	P51828 homo sapien
24	39	43.8	471	1	YX11_CABEL	Q11122 canenorhabditis elegans
25	39	43.8	581	1	YG25_ARCFU	P08648 archaeoglobaceae
26	39	43.8	866	1	II7R_HUMAN	Q96f46 homo sapien
27	39	43.8	1607	1	MIFP_LMNST	P25410 lymnaea stagnalis
28	38.5	43.3	488	1	HDA2_CHICK	P256519 gallus gallus gallus gallus
29	38.5	43.3	488	1	HDA2_HUMAN	P02769 homo sapien
30	38.5	43.3	488	1	HDA2_MOUSE	P70288 mus musculus
31	38	42.7	214	1	VIF_SIVML	P05903 simian immuno
32	38	42.7	214	1	VIF_SIYMK	P12502 simian immuno
33	38	42.7	214	1	VIF_SIVS4	P12505 simian immuno

ALIGNMENTS

RESULT 1
CP72_CATRO
ID CP72_CATRO
AC 005047;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome P450 72A1 (EC 1.14.14.1) (CYPLXXII) (Secologanin synthase)
(SUL).
GN CYP72A1 OR CYP72 OR P450CR3.
OS Catharanthus roseus (Rosy Periwinkle) (Madagascar periwinkle),
OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
OC Vincineae; Catharanthus.

NCBI TaxID=4058;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV, CP3A;
RC Vetter H.-P., Mangold U., Schroeder G., Marner F.-J.,
RA Werck-Reichhart D., Schroeder J.;
RT "Molecular analysis and heterologous expression of an inducible cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).";
RT cytochrome P-450 protein from periwinkle (Catharanthus roseus L.).
RN [2]
RN SEQUENCE OF 469-524 FROM N.A.
RP STRAIN=CV, G. Don;
RC MEDLINE=3283641; PubMed=8507838;
RX Meijer A.H., Souer E., Verpoort R., Hoge J.H.C.;
RA RT "Isolation of cytochrome P-450 cDNA clones from the higher plant Catharanthus roseus by a PCR strategy.;"
RT Plant Mol. Biol. 22:379-383(1993).
RL [3]
RN FUNCTION.
RP STRAIN=CV, CPA;
RC MEDLINE=20575713; PubMed=11135113;
RX Trmler S., Schroeder G., St-Pierre B., Crouch N.P., Hotze M.,
RA Schmidt J., Strack D., Matern U., Schroeder J.;
RA RT "Indole alkaloid biosynthesis in Catharanthus roseus: new enzyme activities and identification of cytochrome P450 CYP72A1 as seco-loganin synthase."
RT Plant J. 24:797-804(2000).
RL [4]
RN -!- FUNCTION: Converts loganin into seco-loganin.
CC -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH + oxidized flavoprotein + H(2)O.
CC -!- PATHWAY: INDOLE ALKALOID SYNTHESIS.
CC -!- SUBCELLULAR LOCATION: Vacuolar membrane (Probable).
CC -!- TISSUE SPECIFICITY: Upper and lower leaf epidermis.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC	CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN (BY SIMILARITY).	Qy	1 WEYLNTWETCER 13
CC	-!- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY SIMILARITY).	Db	334 WIVAATVYRCER 346
CC	-!- ALTERNATEULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	RESULT 4	KCN1_HUMAN
CC	-!- ALTERNATIVE PRODUCTS: AT LEAST 16 ISOFORMS ARE PRODUCED RESULTING FROM THE DIFFERENTIAL SPLICING OF AT LEAST 12 EXONS.	ID	KCN1_HUMAN
CC	-!- TISSUE SPECIFICITY: WIDELY EXPRESSED INCLUDING BRAIN.	STANDARD;	PRT;
CC	-!- POLYMORPHISM: THE POLY GLU REGION OF KCNN1 IS POLYMORPHIC AND THE NUMBER OF GLN VARIES BETWEEN STRAINS (FROM 10 TO 12). THE REPEAT WITH 10 GLU RESIDUES (SHOWN HERE) IS FOUND IN BALB/C, DBA/2J, 129/SVJ, AJ, C3H/HeJ, BALB/CJ, BXD-31, SM/J, ST/Ba, FVB/NJ,	AC	092952;
CC	NCBZ/BINJ, CBA/J AND CAST/B1.	DT	15-JUN-2002 (Rel. 41; Created)
CC	-!- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS	DT	15-JUN-2002 (Rel. 41; Last sequence update)
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	DE	Small conductance calcium-activated potassium channel protein 1 (SK1).
CC	EMBL: AF116525; AGA43216; 1; -.	GN	KCNN1 OR SK1.
CC	EMBL: AF297869; AAK30363; 1; JOINED.	OS	Homo sapiens (Human).
CC	EMBL: AF303461; AAK29550; 1; -.	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC	EMBL: AF303462; AAK29551; 1; -.	OX	NCBI_TaxId:9606;
CC	EMBL: AF303463; AAK29552; 1; -.	RN	OX
CC	EMBL: AF357239; AAK48900; 1; -.	RP	SEQUENCE FROM N.A.
CC	HSSP: P70604; 1; G4Y.	RC	SEQUENCE FROM N.A.
CC	MGI: MGI_1933933; Kcnn1.	RA	TISSUE=Hippocampus;
CC	DR InterPro: IPR014178; CamBp.	RT	Medline=93776602; PubMed=8781233;
CC	DR InterPro: IPR016222; K+channel_pore.	RA	Koehler M., Hirschberg B., Bond C.T., Kinzie J.M., Marion N.V.,
CC	DR InterPro: IPR003931; SK_channel.	RT	Maylie J., Adelman J.P.;
CC	PFam: PF02888; CamBp; 1.	RL	"Small-conductance, calcium-activated potassium channels from mammalian brain";
CC	PFam: PF05350; SK_channel; 1.	CC	Science 27:1709-1714 (1996).
CC	Ionic channel; Transmembrane; Ion transport; Calmodulin-binding;	RN	111
CC	KW Alternative splicing; Polymorphism.	RP	SEQUENCE FROM N.A.
CC	FT TRANSMEM 151 171 SEGMENT S1 (POTENTIAL).	RX	Medline=99474612; PubMed=10516139;
CC	FT TRANSMEM 180 200 SEGMENT S2 (POTENTIAL).	RA	Litt M., LaMorticella D., Bond C.T., Adelman J.P.;
CC	FT TRANSMEM 219 239 SEGMENT S3 (POTENTIAL).	RT	Gene structure and chromosome mapping of the human small-conductance calcium-activated potassium channel SK1 gene (KCNN1).";
CC	FT TRANSMEM 268 288 SEGMENT S4 (POTENTIAL).	RA	Cytogenet. Cell Genet. 86:70-73 (1999).
CC	FT TRANSMEM 317 337 SEGMENT S5 (POTENTIAL).	RT	"FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE HYPERPOLARIZATION, THOUGHT TO REGULATE NEURONAL EXCITABILITY BY CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN SUBUNITS: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM BINDING (BY SIMILARITY).
CC	FT DOMAIN 357 377 SEGMENT H5 (PORE-FORMING) (POTENTIAL).	CC	"SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	FT DOMAIN 386 406 SEGMENT S6 (POTENTIAL).	CC	"SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
CC	FT DOMAIN 107 118 POLY GLU.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	FT DOMAIN 424 503 CALMODULIN-BINDING (BY SIMILARITY).	CC	CC
CC	FT VARSPLIC 1 43 MISSING (IN EXON A/3.2 OR C/B/3.2).	CC	CC
CC	FT VARSPLIC 394 430 MISSING (IN EXON 6/8).	CC	CC
CC	FT VARSPLIC 466 580 KFLQAIHQACKLRLQKLNQDNLIAELAKAQSIAYE VVSLEQAOQFELEARLALESRLDVLGASLQLPQIADAI CPLPPWPQPGFLATTHSQSHWLPTMGSDCG -> ERSS	CC	CC
CC	FT VARSPLIC 474 476 EV (IN EXON 8/10).	DR	DR
CC	FT VARSPLIC 109 109 KFLQAIHQACKLRLQKLNQDNLIAELAKAQSIAYE VVSLEQAOQFELEARLALESRLDVLGASLQLPQIADAI CPLPPWPQPGFLATTHSQSHWLPTMGSDCG -> SEV (IN EXONS 8/10).	DR	EMBL; AF131948; AAD37507.1; JOINED.
CC	FT VARIANT 109 109 MISSING (IN EXON 8A/10).	DR	EMBL; AF131941; AAD37507.1; JOINED.
CC	FT VARIANT 109 109 E -> E (IN STRAINS C57Bl/6J, A/HEJ AND SPRET/El).	DR	EMBL; AF131942; AAD37507.1; JOINED.
CC	FT VARIANT 109 109 E -> EEE (IN STRAINS SWR/J, AKR/J, RBF/DN AND P/J).	DR	EMBL; AF131943; AAD37507.1; JOINED.
CC	FT VARIANT 565 565 H -> Q (IN C57BL/6).	DR	EMBL; AF131944; AAD37507.1; JOINED.
CC	FT VARIANT 580 AA; 64066 MW; 7B30C8A28B349C80 CRC64;	DR	EMBL; AF131945; AAD37507.1; JOINED.
SQ	SEQUENCE Best Local Similarity 48.3%; Score 43; DB 1; Length 580; Matches 7; Conservative 53.8%; Pred. No. 41; 0; Gaps 0;	DR	EMBL; AF131946; AAD37507.1; JOINED.
SQ	SEQUENCE 580 Mismatches 6; Indels 0;	DR	EMBL; AF131947; AAD37507.1; JOINED.
SQ	SEQUENCE 580 Gaps 0;	DR	HSSP; P70604; 1G4Y.
SQ	SEQUENCE DR MIM: 602982; -	DR	DR
SQ	SEQUENCE InterPro: IPR004178; CamBp.	DR	InterPro: IPR001622; K+channel_pore.
SQ	SEQUENCE InterPro: IPR003931; SK_channel.	DR	InterPro: IPR003931; SK_channel.
SQ	SEQUENCE Pfam: PF02888; CamBp.	DR	Pfam; PF05350; transmembrane; ion transport; calmodulin-binding.
SQ	SEQUENCE Transm	KW	Transm

FT	TRANSMEM	129	149	SEGMENT S1 (POTENTIAL).	FT	METAL	274	NICKEL 1 (BY SIMILARITY).
FT	TRANSMEM	158	178	SEGMENT S2 (POTENTIAL).	FT	METAL	362	NICKEL 2 (BY SIMILARITY).
FT	TRANSMEM	197	217	SEGMENT S3 (POTENTIAL).	FT	ACT_SITE	322	BY SIMILARITY.
FT	TRANSMEM	246	266	SEGMENT S4 (POTENTIAL).	FT	SEQUENCE	322	IC720A254335D7FD CR64;
FT	TRANSMEM	295	315	SEGMENT S5 (POTENTIAL).	Query	Match	569 AA;	61037 MW;
FT	DOMAIN	335	355	SEGMENT H5 (PORE-FORMING) (POTENTIAL).	Best Local	Similarity	47.28;	Score 42;
FT	TRANSMEM	364	384	SEGMENT S6 (POTENTIAL).	Matches	6;	Length 569;	DB 1;
FT	DOMAIN	402	481	CALMODULIN-BINDING (BY SIMILARITY).	Conservative	3;	Pred. No. 55;	Mismatches
FT	SEQUENCE	527	536	POLY-PRO	Indels	0;	Gaps	0;
SO	SEQUENCE	561 AA;	61826 MW;	66CAA2105FFDE74 CRC64;	Matches	6;	Indels	0;
Query	1	WEVLCTWETCER 13	47.28;	Score 42;	Length 561;	RESULTS	6	KCN2_MOUSE
Best Local	Similarity	46.28;	Pred. No. 54;	DB 1;	Mismatches	1;	STANDARD:	PRT;
Matches	6;	Conservative	1;	Indels	0;	574 AA.	ID: KCN2_MOUSE	PRT;
Db	312 WLTAAATVRCER 324						AC: P58190;	
RESULT 5							DT: 15-JUN-2002 (Rel. 41, Created)	
UREL_SYN3	STANDARD;	PRT;	569 AA.				DT: 15-JUN-2002 (Rel. 41, Last sequence update)	
AC	P73061;	01-NOV-1997 (Rel. 35, Created)					DT: 15-JUN-2002 (Rel. 41, Last annotation update)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)							
DT	15-JUN-2002 (Rel. 41, Last annotation update)							
DE	urease alpha subunit (EC 3.5.1.5) (urea amidohydrolase).							
DE	urease alpha subunit (EC 3.5.1.5) (urea amidohydrolase).							
GN	URBC OR SLL750.							
OS	Synechocystis sp. (strain PCC 6803)							
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.							
OX	NCBI_TaxID=1148;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RX	MEMLINE-97061201; PubMed=8905231;							
RA	Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirose M., Sugiyama M., Sasamoto S., Kimura T., RA Matsuno A., Muraki A., Naruo K., Nakazaki N., Wada T., Watanabe K., Okumura S., Shimpou S., Takeuchi C., Yamada M., Yasuda M., Tabata S.; RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein coding regions."; RA DNA Res. 3:109-116(1996).							
CC	- - CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).							
CC	- - COFACTOR: Blinds 2 nickel ions per subunit (BY similarity).							
CC	- - SUBUNIT: (ALPHA, BETA, GAMMA) (3). (BY SIMILARITY).							
CC	- - PTM: Lys-219 is carbonylated. The carbonyl group provides the ligands for the two nickel ions (BY similarity).							
CC	- - SIMILARITY: BELONGS TO THE UREASE FAMILY.							
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CC	EMBL; D90903; BAA17083.1; -							
CC	HSSP; P18314; IWF.							
CC	DR MEROPS; M38 UNW; -							
CC	DR InterPro; IPR01924; UreaseA.							
CC	DR Pfam; PF00449; urease.C; 1.							
CC	DR Pfam; PF02802; urease.C; 1.							
CC	DR PRODOM; P002467; UreaseA; 1.							
CC	DR PROSITE; PS00145; UREASE_2; 1.							
CC	DR PROSITE; PS01120; UREASE_1; 1.							
CC	KW Hydrolase; Metal-binding; Nickel; Complete proteome.							
FT	METAL	136	136	NICKEL 2 (BY SIMILARITY).	FT	TRANSMEM	340	SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT	METAL	138	138	NICKEL 2 (BY SIMILARITY).	FT	TRANSMEM	369	SEGMENT S6 (POTENTIAL).
FT	METAL	219	219	NICKEL 1 AND 2 (BY SIMILARITY).	FT	DOMAIN	407	CALMODULIN-BINDING (BY SIMILARITY).
FT	METAL	248	248	NICKEL 1 (BY SIMILARITY).	FT	DOMAIN	42	POLY GLY.

FT DOMAIN 52 56 POLY-ALA.
 FT DOMAIN 80 85 POLY-GLY.
 FT DOMAIN 88 97 POLY-GLY.
 FT DOMAIN 558 561 POLY-ARG.
 SQ SEQUENCE 574 AA: 63482 MW; 259CB8CDE4D1CDE6 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 574;
 Best Local Similarity 46.2%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEYLWTWETCER 13
 ID KCN2_HUMAN STANDARD; PRT: 579 AA.
 AC 091251;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Small conductance calcium-activated potassium channel protein 2 (SK2).
 GN KCNN2.
 OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Primates; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX NCBI_TaxID=9606; [1]

RN SEQUENCE FROM N.A.
 RX MEDLINE=20568244; PubMed=10991935;
 RA "Characterization of calcium-activated potassium channels in human
 membrane.", NCBITaxon=10116;

RT Submitted (JUL-2001) to the EMBL/GenBank/DBJU databases.
 CC -!- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED
 BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE
 HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY
 CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC
 AFTERHYPERPolarization. THE CHANNEL IS BLOCKED BY APAMIN.
 CC -!- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
 I SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
 REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
 SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -!- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC DR EMBL: AF239613; AAG16728; 1; -.
 CC DR EMBL: AF39715; ARK84039; 1; -.
 CC DR HSSP: P70604; 1G4Y.
 CC DR Genew: HGNC:3291; KCNN2.
 CC DR MIM: 603879; -.
 CC DR InterPro: IPRO04178; CAMBD.
 CC DR InterPro: IPRO01622; K+channel_pore.
 CC DR Pfam: PF02888; CaUBD; 1.
 CC DR Pfam: PF03530; SK_channel; 1.
 CC DR Pfam: PF03530; SK_channel; 1.

KW Ionic channel; Transmembrane; Ion transport; Calmodulin-binding.
 FT TRANSMEM 138 158 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 168 188 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 214 234 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 256 276 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 305 325 SEGMENT S5 (POTENTIAL).
 FT TRANSMEM 345 365 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 374 394 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 412 488 CALMODULIN-BINDING (BY SIMILARITY).
 FT DOMAIN 41 45 POLY-GLY.
 FT DOMAIN 51 58 POLY-ALA.
 FT DOMAIN 83 88 POLY-GLY.
 FT DOMAIN 91 102 POLY-GLY.
 FT DOMAIN 563 566 POLY ARG.
 FT CONFLICT 52 52 D -> AA (IN REF. 2).
 FT CONFLICT 323 323 I -> T (IN REF. 2).
 FT CONFLICT 530 530 Q -> R (IN REF. 2).
 SQ SEQUENCE 579 AA; B1DAE3513C1061B2 CRC64;

RESULT 7
 KCN2_RAT STANDARD; PRT: 580 AA.
 AC P70604;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Small conductance calcium-activated potassium channel protein 2 (SK2).
 GN KCNN2.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus .
 OX NCBITaxon=10116;

Query Match 47.28%; Score 42; DB 1; Length 579;
 Best Local Similarity 46.2%; Pred. No. 56;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEYLWTWETCER 13
 Db 322 WIIAWTVRACER 329

RESULT 8
 KCN2_RAT STANDARD; PRT: 580 AA.
 AC P70604;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small conductance calcium-activated potassium channel protein 2 (SK2).
 GN KCNN2.
 OS Rattus norvegicus (Rat).
 OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus .
 OX NCBITaxon=10116;

SEQUENCE FROM N.A.
 RX MEDLINE=93376602; PubMed=8781233;
 RN SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC Koehler M., Hirschberg B., Bond C.T., Kinzie J.M., Marrion N.V.,
 RX MEDLINE=93376602; PubMed=8781233;
 RA "Small-conductance, calcium-activated potassium channels from
 RT mammalian brain";
 RT Science 273:1709-1714(1996).
 RN [2]
 RP INTERACTION WITH CALMODULIN.
 RX MEDLINE=9845090; PubMed=9774106;
 RA Xia X.M., Fakler B., Rivard A.F., Wayman G., Johnson-Pais T., Keen J.E., Ishii T., Hirschberg B., Bond C.T., Lutsenko S., Maylie J.,
 RA Adelman J.P.; Schumacher M.A., Rivard A.F., Bachinger H.P., Adelman J.P.;
 RA "Structure of the gating domain of a Ca2+-activated K+ channel
 complexed with Ca2+/calmodulin.";
 RN Nature 395:503-507 (1998).
 [3]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 395-490 WITH CALMODULIN.
 RX MEDLINE=21223356; PubMed=11322678;
 RA Schumacher M.A., Rivard A.F., Bachinger H.P., Adelman J.P.;
 RA "Mechanism of calcium gating in small-conductance calcium-activated
 potassium channels";
 RT Nature 410:1120-1124 (2001).
 RN [4]
 RP FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED
 BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE
 HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY
 CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC
 AFTERHYPERPolarization. THE CHANNEL IS BLOCKED BY APAMIN.
 CC -!- FUNCTION: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
 CC -!- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL
 I SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH
 REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY
 SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -!- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.

CC REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN.

CC -1- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.

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DR EMBL; U69882; AAB09563; 1;
 DR InterPro; IPR04178; CamBD.
 DR InterPro; IPR01622; K+channel_pore.
 DR Pfam; PF02888; CamBD; 1.
 DR Pfam; PF03530; SK_channel; 1.
 KW Ionic channel; Transmembrane; Ion transport; Calmodulin-binding;

KW 3D-structure.

FT TRANSMEM 140 160 SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 169 189 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 215 235 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 257 277 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 306 326 SEGMENT S5 (POTENTIAL).
 FT TRANSMEM 346 366 SEGMENT H5 (POTENTIAL).
 FT TRANSMEM 375 395 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 413 489 CALMODULIN-BINDING.
 FT DOMAIN 42 46 POLY-GLY.
 FT DOMAIN 52 56 POLY-ALA.
 FT DOMAIN 80 85 POLY-GLY.
 FT DOMAIN 88 103 POLY-ARG.
 FT DOMAIN 564 567 MW; F71EDDAF7BEFA8D4 CRC64;
 SQ SEQUENCE 580 AA; 63847 MW;

Query Match Best Local Similarity 47.2%; Score 42; DB 1; Length 724;
 Matches 6; Conservative 46.2%; Pred. No. 56; Gaps 0;

Qy 1 WEVLCTWTCER 13
 Db 323 WITAAWTVRACER 335

RESULT 9

KCN3_PIG	ID	KCN3_STANDARD	PRT	724 AA.
AC P50392;	DT 15-JUN-2002 (Rel. 41, Created)			
DE	DT 15-JUN-2002 (Rel. 41, Last sequence update)			
GN KCNN3	DE Small conductance calcium-activated potassium channel protein 3 (SK3).			
OS Sus scrofa (Pig).				
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCBI_TaxID=9823;				
OX				
RN				
RC TISSUE=Coronary artery.				
RA MEDLINE=21866175; PubMed=11877319;				
RA Weston M.P., Bychkov R., Feletou M., Richards G.R., Vanhoutte P.M., Edwards G.;				
RT "Characterization of an apamin sensitive small-conductance Ca(2+)-activated K(+)-channel in porcine coronary artery endothelium: relevance to EDHF." Br. J. Pharmacol. 135:1133-1143 (2002).				
RL	-1- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE HYPERPOLARIZATION, THOUGHT TO REGULATE NEURONAL EXCITABILITY BY CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC			

CC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN (BY SIMILARITY).
 CC -1- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH REGULATES THE CHANNEL ACTIVITY THROUGH CALCTUM-BINDING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.
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 CC or send an email to license@isb-sib.ch).

CC DR EMBL; AY038049; AAC71498; 1;
 CC DR InterPro; IPR004178; CamBD.
 CC DR Interrr; IPR001622; K+channel_pore.
 CC DR InterPro; IPR03931; SK_channel.

DR Pfam; PF02888; CamBD; 1;
 DR Pfam; PF0530; SK_channel; 1.
 DR Ionic channel; Transmembrane; Ion transport; Calmodulin-binding.
 KW SEGMENT S1 (POTENTIAL).
 FT TRANSMEM 281 301 SEGMENT S2 (POTENTIAL).
 FT TRANSMEM 308 328 SEGMENT S3 (POTENTIAL).
 FT TRANSMEM 359 379 SEGMENT S4 (POTENTIAL).
 FT TRANSMEM 398 418 SEGMENT S5 (POTENTIAL).
 FT TRANSMEM 447 467 SEGMENT S6 (POTENTIAL).
 FT TRANSMEM 487 507 SEGMENT H5 (PORE-FORMING) (POTENTIAL).
 FT TRANSMEM 516 536 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 554 630 CALMODULIN-BINDING (BY SIMILARITY).
 FT DOMAIN 30 34 POLY-GLN.
 FT DOMAIN 35 45 POLY-PRO.
 FT DOMAIN 62 73 POLY-GLN.
 FT DOMAIN 141 146 POLY-GLY.
 FT DOMAIN 676 680 POLY-GLN.
 FT DOMAIN 720 723 POLY-SER.
 SQ SEQUENCE 724 AA; AFPF6894935Ba4196F CRC64;
 Query Match Best Local Similarity 47.2%; Score 42; DB 1; Length 724;
 Matches 6; Conservative 46.2%; Pred. No. 68; 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCTWTCER 13
 Db 464 WITAAWTVRACER 476

RESULT 10

KCN3_MOUSE	ID	KCN3_STANDARD	PRT	731 AA.
AC P58351;	DT 15-JUN-2002 (Rel. 41, Created)			
DE	DT 15-JUN-2002 (Rel. 41, Last sequence update)			
GN KCNN3 OR SK3	DT 15-JUN-2002 (Rel. 41, Last annotation update)			
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus (Mouse).	DE Small conductance calcium-activated potassium channel protein 3 (SK3).			
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.	GN KCNN3_MOUSE			
OX	RN [1] FROM N.A.			
RN	RP SEQUENCE=BALB/C; TISSUE=Colon;			
RC	RC MEDLINE=21440583; PubMed=11557517;			
RA	RA RO S.; Hatton W.J.; Koh S.D.; Horowitz B.;			
RT	RT "Molecular properties of small-conductance Ca2+-activated K+ channels expressed in murine colonic smooth muscle." Am. J. Physiol. 281:G964-G973 (2001).			
RT	-1- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY			
CC	CC			
CC	CC			

CONTRIBUTING TO THE SLOW COMPONENT OF SYNAPTIC AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN (BY SIMILARITY).

-1- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.

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EMBL; AF57241; AAK48902; 1;

DR InterPro; IPR004178; CaMBD.

DR InterPro; IPR001622; K+channel_pore.

DR Pfam; PF02888; CaMBD; 1.

DR Pfam; PF03550; SK_Channel; 1; Ion transport; Calmodulin-binding.

KW Ionic channel; Transmembrane; Calmodulin-binding.

FT TRANSMEM 288 308 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 315 335 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 366 386 SEGMENT S3 (POTENTIAL).

FT TRANSMEM 405 425 SEGMENT S4 (POTENTIAL).

FT TRANSMEM 454 474 SEGMENT S5 (POTENTIAL).

FT TRANSMEM 494 514 SEGMENT H5 (PORE FORMING) (POTENTIAL).

FT TRANSMEM 523 543 SEGMENT S6 (POTENTIAL).

FT DOMAIN 561 637 CALMODULIN-BINDING (BY SIMILARITY).

FT DOMAIN 30 43 POLY-PRO.

FT DOMAIN 36 43 POLY-GLN.

FT DOMAIN 60 79 POLY-GLN.

FT DOMAIN 683 687 POLY-SER.

FT DOMAIN 727 730 POLY-SER.

SEQUENCE 731 AA: 81255 MW: E509C97E975C1A42 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 731; Best Local Similarity 46.2%; Pred. No. 68; Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

RESULT 11

KCN3_RAT STANDARD; PRT; 732 AA.

ID KCN3_RAT P7605; Q9E011; Q9ERQ4; 483

Db 471 WIATAANTVRVCER 483

DE Small conductance calcium-activated potassium channel protein 3 (SK3).

GN KCN3 OR SK3

OS Rattus norvegicus (Rat).

OC Eubaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

NCB_TaxID=10116;

RN SEQUENCE FROM N.A.

STRAIN=Sprague-Dawley; TISSUE=Brain; MEDLINE=21424375; PubMed=11533126;

RA Hosseini R.; Benton D.C.; Dunn P.M.; Jenkinson D.H.; Moss G.W.; RT "SK3 is an important component of K(+) channels mediating the afterhyperpolarization in cultured rat SCG neurones.";

RL J. Physiol. (Lond.) 535:323-334 (2001).

RN [3]

SEQUENCE FROM N.A. AND VARIANT 78-GLN-GLN-79 DEL.

RP STRAIN=Sprague-Dawley; TISSUE=Liver;

RC MEDLINE=2143871; PubMed=11245600;

RX RA Barford E.T.; Moore A.L.; Lidofsky S.D.;

RT "Cloning and functional expression of a liver isoform of the small conductance Ca2+-activated K⁺ channel SK3".

RT RL Am. J. Physiol. 280(C836-C842)(2001)

-1- FUNCTION: FORMS A VOLTAGE-INDEPENDENT POTASSIUM CHANNEL ACTIVATED BY INTRACELLULAR CALCIUM. ACTIVATION IS FOLLOWED BY MEMBRANE HYPERPOLARIZATION. THOUGHT TO REGULATE NEURONAL EXCITABILITY BY CONTRIBUTING TO THE SLOW COMPONENT SYNAPtic AFTERHYPERPOLARIZATION. THE CHANNEL IS BLOCKED BY APAMIN.

CC -1- SUBUNIT: HETERO-OLIGOMER. THE COMPLEX IS COMPOSED OF 4 CHANNEL SUBUNITS EACH OF WHICH BINDS TO A CALMODULIN SUBUNIT WHICH REGULATES THE CHANNEL ACTIVITY THROUGH CALCIUM-BINDING (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE KCNN FAMILY OF POTASSIUM CHANNELS.

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EMBL; U69884; AAB81653; 1;

DR EMBL; AF292389; AAC13967; 1;

DR EMBL; AF24345; AAC38878; 1;

DR HSSP; P70504; 1G4Y.

DR InterPro; IPR004178; CatBD.

DR InterPro; IPR001622; K+channel_pore.

DR Pfam; PF02888; Camb; 2.

DR Pfam; PF05330; SK_channel; 1;

KW Ionic channel; Transmembrane; Ion transport; Calmodulin-binding;

FT TRANSMEM 289 309 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 316 336 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 367 387 SEGMENT S3 (POTENTIAL).

FT TRANSMEM 406 426 SEGMENT S4 (POTENTIAL).

FT TRANSMEM 455 475 SEGMENT S5 (POTENTIAL).

FT TRANSMEM 495 515 SEGMENT H5 (PORE-FORMING) (POTENTIAL).

FT TRANSMEM 524 544 SEGMENT S6 (POTENTIAL).

FT DOMAIN 562 638 CALMODULIN-BINDING (BY SIMILARITY).

FT DOMAIN 30 35 POLY-GLN.

FT DOMAIN 36 39 POLY-GLN.

FT DOMAIN 60 80 POLY-GLN.

FT DOMAIN 684 688 POLY-GLN.

FT VARIANT 728 731 POLY-SER.

FT MISSING. 78 79

FT CONFLICT 9 9 D -> E (IN REF. 1).

FT CONFLICT 96 96 L -> V (IN REF. 1).

FT CONFLICT 138 138 L -> V (IN REF. 1).

FT CONFLICT 162 162 L -> V (IN REF. 1).

FT CONFLICT 190 190 S -> N (IN REF. 1).

SEQUENCE 732 AA: 81448 MW: C44579B78EFB0ADA CRC64;

Query Match 47.2%; Score 42; DB 1; Length 732; Best Local Similarity 46.2%; Pred. No. 69; Matches 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 WEVLCWTCER 13

RN | : ||| |||

